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Title:
                                                                                                                                                                                Database :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2427
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pir2:*
pir3:*
pir4:*
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RESULT 1

G2MS11

Ig gamma-2b chain - mouse

C; species: Mus musculus (house mouse)

C; species: Musculus (house mouse

A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specifi A;Reference number: \$25057 A;Accession: \$25057

A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-474 <FIS>

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42.4	43.2	43.4	43.6	43.6	44.2		44.5	44.5	44.8	45.3	45.8	47.2	. `	47.8	48.2	49.5	53.0	54.4	54.7	57.1	8	œ	59.3	٠.	75.5	<u>ب</u>	88.0	90.3	Match I	,
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Ig gamma	Ig gamma 2b chair	Ig	Ig	Ig gamma-2 chain	Ig gamma-3 chain	Ig gamma-3 chain	gamma-	chain C	gamma-1 c	Ig gamma-2a chain	Ig gamma-1 chain	gamma-1 chain	1	gamma-3 chain	Ig gamma-3 c	Ig gamma	Ig heavy ch	· Ig gamma-1 c	Ig gamma-2b	Ig gamma-2a	Ig gamma-2a	Ig gamma-2a chain	mon	Ig gamma-2b	Ig gamma-2a	Ig gamma-2a	Ig gamma-2b cha	Ig gamma-2b cha	Description	

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	42.2 41.8 41.6 41.7 35.2 35.2 35.2 33.7 32.2 32.1 32.1 31.9
	308 328 548 548 327 377 237 249 549 627 225 221 221 213
	H0000400000000000000000000000000000000
ALIGNMENTS	C30554 17158 S38950 S38864 S06611 S06611 S06611 S147165 PC4155 PC4155 S14845 S14845 S14845 S148220 PC4202 PC4202 S68213 S68213 S70207 G3HUWI
ENTS	,
	Ig heavy chain C r Ig gamma 1 chain c Ig gamma chain - m Ig epsilon chain C Ig gamma-2 chain C Ig gamma-2 chain C Ig heavy chain v r Ig gamma-4 chain c Ig gamma-2b chain c Ig gamma-1b chain c Ig gamma-1b chain C Ig gamma-1 chain (Ma Ig heavy chain (Ma Ig gamma chain C r Ig gamma chain C r

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R;Kim, H.; Yamaayuchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takah J. Biol. Chem. 269, 12345-12350, 1994	A;Accession: A26233 A;Molecule type: DNA A;Residues: 138-61,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <ol< td=""><td>A; TILLO, R.; ROUGEUI, F. Nature 296, 761-763, 1982  A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and g A;Reference number: A26233; MUID:82173203  A;Contents: b allele</td><td>A;Reference number: A26232; MUID:80081502 A;Accession: A26232 A;Molecule type: DNA A;Residues: 138-172,'p',174-189,'FP',193-376,'T',378-474 <tu2></tu2></td><td>A; Residues: 138-172, 'P',174-189, 'FP',193-376, 'T',378-474 <tu1> A; Note: Lys-474 is probably removed posttranslationally R; Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R. Science 206, 1303-1306, 1979 Science 206, 1303-1306, 1979</tu1></td><td>A;Note: the sequence was determined from the germline gene A;Note: the sequence was determined from the germline gene R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R. Science 206, 1299-1303, 1979 A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b A;Reference number: A26235; MUID:80081501 A;Contents: MPC 11 A;Accession: A26235 A;Molecule type: mRNA A;Molecule type: mRNA</td><td>A;Reference number: A02157; MUID:80120716 A;Contents: a allele A;Concession: A02157 A;Molecule type: DNA A;Residues: 138-161,'L',163-189,'FP',193-474 <yam> A:Cross=references: GB:T00461</yam></td><td>A;Cross.references: EMBL:X67210; NID:q54826; PIDN:CAA47649.1; PID:q54827 A;Cross.references: EMBL:X67210; NID:q54826; PIDN:CAA47649.1; PID:q54827 R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T. Nature 283, 786-789, 1980 A;Title: Complete nucleotide sequence of immunoalohulin gamma2b chain gene cloned fro</td></ol<>	A; TILLO, R.; ROUGEUI, F. Nature 296, 761-763, 1982  A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and g A;Reference number: A26233; MUID:82173203  A;Contents: b allele	A;Reference number: A26232; MUID:80081502 A;Accession: A26232 A;Molecule type: DNA A;Residues: 138-172,'p',174-189,'FP',193-376,'T',378-474 <tu2></tu2>	A; Residues: 138-172, 'P',174-189, 'FP',193-376, 'T',378-474 <tu1> A; Note: Lys-474 is probably removed posttranslationally R; Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R. Science 206, 1303-1306, 1979 Science 206, 1303-1306, 1979</tu1>	A;Note: the sequence was determined from the germline gene A;Note: the sequence was determined from the germline gene R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R. Science 206, 1299-1303, 1979 A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b A;Reference number: A26235; MUID:80081501 A;Contents: MPC 11 A;Accession: A26235 A;Molecule type: mRNA A;Molecule type: mRNA	A;Reference number: A02157; MUID:80120716 A;Contents: a allele A;Concession: A02157 A;Molecule type: DNA A;Residues: 138-161,'L',163-189,'FP',193-474 <yam> A:Cross=references: GB:T00461</yam>	A;Cross.references: EMBL:X67210; NID:q54826; PIDN:CAA47649.1; PID:q54827 A;Cross.references: EMBL:X67210; NID:q54826; PIDN:CAA47649.1; PID:q54827 R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T. Nature 283, 786-789, 1980 A;Title: Complete nucleotide sequence of immunoalohulin gamma2b chain gene cloned fro

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A;Introns: 138/1; 236/1; 258/1; 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin cregion; immunoglobulin homology complex in the subunits associate into la C;Superfamily: immunoglobulin homology cimin cregion; immunoglobulin homology cimin cregio
                                                                                                                                          Ig gamma-2b chain precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1989 #sequence_revision 30-Sep C;Accession: S01321 R;de Waele, P.; Feys, V.; van de Voorde, A.; Eur. J. Biochem. 176, 287-295, 1988
                                                                                                                                                                                                                                                                                                                                   RESULT
S01321
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A:Reference number: A53598; MUID:94216359
A:Accession: A53598
A:Status: preliminary
A:Molecule type: protein
A:Molecule type: protein
A:Residues: 234-251 <KIM>
C:Comment: The a allele sequence is shown.
A; Molecule type: mRNA
A; Residues: 1-475 < DE
                                                        A; Title: Expression in non-lymphoid cells of A; Reference number: S01320; MUID:88329081 A; Accession: S01321
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Pred. No. 1.4e-123;
Pred. No. 1.4e-123;
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                                                                                                              mouse recombinant immunoglobulin
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A;Residues: 1-469 <DUC>
A;Residues: 1-469 <DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253 C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin C;Keywords: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                  C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
C:Accession: S37483
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                                                                                                                                                                                                                                                               A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                           Ig gamma-2a
                                                                    Query Match
Best Local Similarity
Matches 345; Conser
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Best Local Similarity
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QIQLQQSGPELVKPGASVKISCKASGYTFTDYYINWVKQKPGQGLKWIGWIYPASGNTKY
                  EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVQLQQSGAELARPGASVKLSCKASGYTLTSYGISWVKQRTGQGLEWIGEIYPGSGNSYF
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                                                                                                                                                                                                                                                                                                                                                                                                           chain - mouse
                                                                    Conservative
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75.7%;
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                                                                                    Score 1835; DB 2; Pred. No. 2.2e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2135; DB 2
Pred. No. 3e-120;
                                                                    Mismatches
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                                                                                                     Length 469;
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A; Map position: 12
C; Superfamily: immunoglobulin C region; immunoglob C; Keywords: disulfide bond; glycoprotein; immunogl. F; 1-446/Product: Ig gamma-2a chain *status experim F; 1-117/Domain: V-D-J region <VDJ>F; 118-446/Domain: C region <CHP>F; 118-244/Domain: C1 region <CHP>F; 118-214/Domain: C1 region <CHP>F; 215-230/Region: hinge
F; 231-340/Domain: C3 region <CH3>F; 241-446/Domain: dimmunoglobulin homology <IMM>F; 241-446/Domain: immunoglobulin homology <IMM>F; 241-446/Domain: dimmunoglobulin homology <IMM>F; 241-446/Domain: d
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C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
C:Accession: S40295
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 ac
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A; Accession: S40295
A; Molecule type: protein
A; Residues: 1-446 <KLE>
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Best Local :
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                                     SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAGAYYFDYWGQGTTLTVSSAK 120
NEKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYFCA-RGGKFAMDYWGQGTSVTVSSAK
                                                                                                                                                                VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
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                                                                                                                              QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLEWIGWIYPGSGNTKY
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                                                                                                                                                                                                                                                                                          Score 1832.5; DE
Pred. No. 3e-102;
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IqA and IgM, the subunits associate int C;Superfamily: immunoglobulin cregion; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunog. F;143-212/Domain: immunoglobulin homology cIMM>
F;370-405/Domain: intracellular #status predicted <IMM>
F;380-369/Domain: intracellular #status predicted <IMM>
F;381-369/Domain: intracellular #status predicted <IMM>
                                                                                                                                                                                                                                                            C;Comment: The sequence of residues 1-334 was assumed to be identical with the corres C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The hat it contains an alternative 3' end, encoded in separate exons, that is homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 335-378 <ROG>
A;Residues: 335-378 <ROG>
A;Note: the translation of the first exon of the membrane-bound segment
A;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:J00462
R;Rogers, J.; Choi, E.; Souza,
Cell 26, 19-27, 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T. Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982 A;Title: Nucleotide sequences of gene segments encoding A;Reference number: A02154; MUID:822222190 A;Accession: C02154
                                                                                                                                                                                                              A; Introns: 1/1; 98/1; 120/1; 230/1; 335/1; 378/3
                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-335, 'K' <YA2>
                                                                                                                                                                                                                                                                                                                                                                                               A; Contents: a allele
A; Accession: B02157
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Complete nucleotide sequence of immunoglobulin A; Reference number: A02157; MUID:80120716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Gene segments encoding transmembrane A; Reference number: A02158; MUID:82115295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig gamma-2b chain C region, membrane-bound form - mouse C;Species: Mus musculus (house mouse) C;Decte: 17-Dec-1982 #sequence_revision 31-Mar-1991 #text_change C;Accession: C02154; A02158; B02157
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A; Residues: 335-405 < YAM>
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F:22/Disulfide bonds: interchain (to 98) #status predicted F:99/Disulfide bonds: interchain (to 109) #status predicted
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A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a A;Reference number: JC5810; MUID:98063277
A;Accession: PC4436
A;Residues: 1-444 < AKA>
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R; Akashi, S.; Kato,
Biochem. Biophys. Re
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                                    THREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYI 357
                                                                                            APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ
                                                                                                                                                                    GLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCP
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 PREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYT
                                                                      VPEVS----SVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQ
                                                                                                                                                                                                                                           SAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQS 177
                                                                                                                                                 DLYTLSSSYTVPSSTWPSETVTCNVAHPASSTKVDKKIVP-----RDC-GCKPC-ICT
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                                                                                                                                                                                                                                                                                                                                                                                                            EVOLOOSGPELVKPGASVMISCRTSAYTFTENTVHWVKOSHGESLEWIGGI---NPYYGG 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN
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Pred. No. 8.5e-79;
8; Mismatches 102;
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               Query Match
Best Local Similarity
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A;Title: Determination of the primary structure of a mouse IgG A;Reference number: A32659; MUID:74175517
A;Rontents: annotation; myeloma protein MOPC 173
A;Rote: this is one paper in a series reporting the sequence;
A;Note: this sequence differs from that shown at a number of p
R;dee Preval, C; Fougereau, M.
Eur. J. Biochem. 30, 452-462, 1972
A;Title: Determination of the primary structure of a mouse gam
A;Reference number: A32660; MUID:73056887
A;Contents: annotation; MOPC 173, disulfide bonds
C;Genetics:
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;15/Disulfide bonds: interchain (to light chain) #status experimental
F;27-82,144-204,250-308/Disulfide bonds: #status experimental
F;107,110,112/Disulfide bonds: interchain (to heavy chain) #status exp
F;180/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                  hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immu F;20-84/Domain: immunoglobulin homology <IM1>
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A,Cross-references: GB:J00470
A;Note: the sequence was determined from the germline gene
A;Note: the sequence was determined from the germline gene
A;Note: the sequence was determined from the germline gene
A;Note: the sequence was determined from the germline gene
A;C: Rougeon, F.
Proc. Natl. Acad. Sci. U.S.A. 78, 2442-2446, 1981
A;Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes suggest
A;Reference number: A32658; MUID:81223894
                                                                                                                                                                                                                                                                                                                                                                                             F;20-84/Domain: immunoglobulin F;98-113/Region: hinge
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C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C; Complex: A)
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A;Molecule type: DNA
A;Residues: 1-330 <OLL>
A;Note: the sequence was determined from the germline
A;Note: Lys-330 is removed posttranslationally
A;Note: Lys-330 is removed posttranslationally
R;Bourgois, A.; Fougereau, M.; Rocca-Serra, J.
Eur. J. Blochem. 43, 423-435, 1974
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R;Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.
Nucleic Acids Res. 9, 1365-1381, 1981
A;Title: The complete nucleotide sequence of mouse
A;Reference number: A32657; MUID:8119876
A;Accession: A32657
A;Molecule type: DNA
A;Residues: 1-330 < NAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-330 <SIK>
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Conservative

30;

Pred. No. 9.400; Mismatches Score 1419; Pred. No. 9

DB 1; 36;

Length 330;

Indels

6,

Gaps

2;

58.5%; 78.6%;

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A; Molecule type: DNA
A; Residues: 329-399 < YAM>
A; Cross-references: GB: J00471
A; Note: the sequence was determined from the ge:
R; Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.
Nucleic Acids Res. 9, 1365-1381, 1981
A; Title: The complete nucleotide sequence of mol A; Reference number: A32657; MUID: 81198976
A; Accession: B32657
                                                                                                                                          A.Introns: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits assoc
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer;
                                                                                  F;346-363/Domain:
F;364-399/Domain:
                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 373-399 <RES>
A;Residues: 373-399 <RES>
A;Cross-references: GB:M35032; NID:g194478; PIDN:AAA37919.1; PID:g387217
C;Comment: The sequence of residues 1-328 was assumed to be identical with the correspon C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The maint it contains an alternative 3' end, encoded in separate exons, that is homologous with
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Sequence and polyadenylation site determination A; Reference number: 157809; MUID:90097953 A; Accession: 157809
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A; Residues: 1-329, Kr < YA2>
R; Hall, B, Milcarek, C.
MOl. Immunol. 26, 819-826, 1989
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A;Title: Nucleotide sequences of gene segments encodi.
A;Reference number: A02154; MUID:82222190
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A; Introns: 1/1; 98/1; 114/1;
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                                                                                                                       Keywords: alternative splicing; duplication; 137-206/Domain: immunoglobulin homology <IMM>
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;Species: Mus musculus (house mouse)
;Date: 19-Feb-1944 #sequence_revision 31-Mar-1991 #text_change
;Accession: A02154; B32657; I57809
  Query
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AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 178

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A; Rolecule type: manna, A; Residues: 1-335 (SCH) A; Cross-references: GB:J00479
A; Cross-references: GB:J00479
A; Experimental source: strain C57BL/6
R; Dognin, M.J; Lauwereys, M.; Strosberg, A.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 4031-4035, 1981
A; Title: Multiple amino acid substitutions between murine gamma 2a heavy chain Fc IA; Title: Multiple amino acid substitutions between murine gamma 2a heavy chain Fc IA; Title: Multiple amino acid substitutions between murine gamma 2a heavy chain Fc IA; Title: Multiple amino acid substitutions between murine gamma 2a heavy chain Fc IA; Title: Multiple amino acid substitutions between murine gamma 2a heavy chain Fc IA; Title: Multiple amino acid substitutions between murine gamma 2a heavy chain Fc IA; A; Close number: A32656; MUID:82037777
A; Reference number: A5303773747
A; Reference number: A5303-334 cDGs
A; Reference number: A32656; MUID:82037777
A; Reference number: A503-334-20324
A; Reference number: A503-334-20324
A; Reference number: A32656; MUID:82037777
A; Reference number: A32656; MUID:82
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Score 1385.5; DB
Pred. No. 9.5e-76;
3; Mismatches 43
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A; Molecule type: DNA
A; Residues: 1-333 <BRU>
A; Residues: 1-333 <BRU>
A; Residues: 1-333 <BRU>
A; Residues: 1-354 | Diamond, A.; Howard, J.; Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Broc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A; Title: Immunoglobulin heavy chain locus of the rat A; Reference number: A25941; MUID:86287397
A; Recension: B25941
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 227-333 <BR2>
C; Genetics:
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C;Superfamily: immunoglobulin C region;
C;Keywords: immunoglobulin
F;20-82/Domain: immunoglobulin homology
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ps00118
rg gamma-2b chain C region - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Jul-1999
C;Accession: PS0018; B25941
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Gene 74, 473-482, 1988
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PREEQYNSTFRVVSALPIQHQDWMSGKEFKCKVNNKALPSPIEKTISKPKGLVRKPQVYV
                                                                                                         THREDYNSTIRVYSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYI
                                                                                                                                                                                                                                                                                                            LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLE-PSGPISTINPCPPCKECHKCP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQKSTWERGSLFACSVVHEVLHNHLTTKTISRSLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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C;Species: Ovis orientalis aries, Ovis an
C;Date: 13-Jan-1995 #sequence_revision 13
C;Accession: S31459
R;Patri, S.; Nau, F.
submitted to the EMBL Data Library, Decen
A;Reference number: S31459
A;Reference number: S31459
A;Recession: S31459
A;Accession: S31459
A;Caccession: S31459
A;Cacc
                                                           Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine N;Alternate names: Ig gamma-1 chain C region (clone 8.10) C;Species: Bos primigenius taurus (cattle) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_C;Accession: $22080; $06610; A31303 R;Sanders, P.G.
A; Reference number: A; Accession: S22080
                    submitted to the EMBL Data Library, A; Reference number: S22080
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C;Superfamily: immunoglobulin C region; immunog C;Kupwords: immunoglobulin
C;Keywords: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                         SYFLYSRLRVDKNSWQEGDTYACVVMHEALHNHYTQKSISKPPGK
                                                                                                                                                                                                                                                                                                                SYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                   APQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNG--HTEENYKDTAPVLDSDG 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVR
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                                                                                                                                                                                                                                                                                                                                                                            EPQVYVLAPPQEELSKSTLSVTCLVTGFYPDYIAVEWQKNGQPESEDKYGTTTSQLDADG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVRLQESGPSLATLLQTLSVTCTISGFSLNNYGVDWVRQAPGKALEWLGG-SGYDEDIDY
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Pred. No. 9.36
                                             November
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Gaps

.80

76 60

351

307 291

367

248 231 196 136

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Ig gamma-2c chain C region - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #te
C;Accession: S00847
R;Brueggemann, M.; DeLmastro-Galfre, P.; Waldmann, H.;
Eur. J. Inmunol. 18, 317-319, 1988
A;Title: Sequence of a rat immunoglobulin gamma-2c hea
A;Reference number: S00847; MUID:88166903
A;Accession: S00847
A;Accession: S00847
A;Accession: S00847
A;Accession: S00847
A;Accession: S00847
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A; Residues: 142-470 < SYM>
A; Residues: 142-470 < SYM>
A; Roross-references: EMBL:X16701
A; Note: the sequence was determined from the germline gene
C; Genetics:
A; Genetics:
A; Genetics:
C; Genetics:
A; Genetics:
A;
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A;Title: Structure of bovine immunoglobulin A;Reference number: 506610, MUID:90097956
A;Accession: S06610
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A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP
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         NID:g57602; PIDN:CAA30169.1;
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Pred. No. 1.1e-69;
0; Mismatches 121;
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      PID: g663228
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light ( C;Complex: An immunoglobulin home cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl C;Reywords: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig gamma-3 chain C region, secreted form - mouse C;Species: Mus musculus (house mouse) C;Date: 17-Mar-1987 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999 C;Accession: B02156 R;Wels, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker. EMBO J. 3, 2041-2046, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: immunoglobulin C region; C;Keywords: immunoglobulin F;20-84/Domain: immunoglobulin homology
                                                                       밁
                                                                                                      Qy
                                                                                                                                                                                                                                                        F;136-205/Domain:
F;242-309/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Structure analysis of the murine A;Reference number: A02156; MUID:85027161
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A; Residues: 1-329 <WEL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB:J00451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 229; Conserv
                                                                                                                                               Matches
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                                                                                        121 TTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLY 180
62
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                                                                                                                                                                  Local
                                                                      N
                  TMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPAPN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPA 238
SLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPR-----IPKPSTPPGSSCPPGN 115
                                                                      TTAPSVYPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQSGFY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDTDSWMRGDIYTCSVVHEALHNHHTQKNLSRSPGK
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                                                                                                                                              221;
                                                                                                                                                                Similarity
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immunoglobulin homology <IM3>
site: carbohydrate (Asn) (cov
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                                                                                                                                                               Score 1170;
Pred. No. 6.
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Pred. No. 7.6
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5.6e-63;
tes 74;
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                                                                                                                                            Gaps
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<u>B</u>1

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A:Introns: 97/1; 113/1; 223/1; 328/1; 371/3
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin C region; immunoglobulin homology C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunog.; j.9-83/Domain: immunoglobulin homology <IM1>
F:97-112/Region: hinge
F:136-205/Domain: immunoglobulin homology <IM2>
F:242-309/Domain: immunoglobulin homology <IM3>
F:242-309/Domain: intracellular #status predicted <IVM>
F:363-398/Domain: intracellular #status predicted <IVM>
F:379,322/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                           Qγ
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A;Title: The structure of the mouse immunoglobulin in gamma-3 membrane general R;Reference number: A02155; MUID:84041483
A;Accession: A02155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig gamma-3 chain C region, membrane-bound form - mouse C:Species: Mus musculus (house mouse) C:Date: 13-Aug-1986 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999 C:Accession: A02155; A02155
R:Wels, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker EMBO J. 3, 2041-2046, 1984
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A; Residues: 1-398 <WEL>
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Best Local Similarity
  116
                            241 LEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHR 300
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                                                                                                                                                                                                                  TTAPSVYPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQSGFY 61
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ILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPRE 175
                                                                                                          SLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPR-----IPKPSTPPGSSCPPGN 115
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                                                                                                                                                                                                                                                                                                                                                            Score 1159; DB 1; Length 398; Pred. No. 3.7e-62;
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